

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2004, 19:35:16 ; Search time 17.0625 Seconds
(without alignments)
39.474 Million cell updates/sec

Title: US-10-618-644-2

Perfect score: 42

Sequence: 1 PNNKPFQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	481	2 S04605	Glycinin G3 - soyb
2	42	100.0	484	2 S11003	Glycinin G3 precu
3	42	100.0	485	1 FWSYG1	Glycinin chain A2B
4	42	100.0	485	2 S11002	Glycinin G2 precu
5	42	100.0	495	1 FWSYG2	Glycinin chain Ala
6	42	100.0	495	2 S10851	Glycinin G1 precu
7	42	100.0	565	1 HMIV51	hemagglutinin prec
8	37	88.1	330	2 JQ2375	hemagglutinin - in
9	37	88.1	330	2 JQ2374	hemagglutinin - in
10	37	88.1	331	2 JQ2378	hemagglutinin - in
11	37	88.1	331	2 JQ2377	hemagglutinin - in
12	37	88.1	347	2 S52186	hemagglutinin - in
13	37	88.1	347	2 S52175	hemagglutinin - in
14	37	88.1	347	2 S52187	hemagglutinin - in
15	37	88.1	347	2 S52183	hemagglutinin - in
16	37	88.1	347	2 S52180	hemagglutinin - in
17	37	88.1	347	2 S52182	hemagglutinin - in
18	37	88.1	347	2 S52179	hemagglutinin - in
19	37	88.1	347	2 S52198	hemagglutinin - in
20	37	88.1	347	2 S52185	hemagglutinin - in
21	37	88.1	347	2 S52189	hemagglutinin - in
22	37	88.1	347	2 S52191	hemagglutinin - in
23	37	88.1	347	2 S52199	hemagglutinin - in
24	37	88.1	347	2 S52178	hemagglutinin - in
25	37	88.1	347	2 S52188	hemagglutinin - in
26	37	88.1	347	2 S52173	hemagglutinin - in
27	37	88.1	347	2 S52174	hemagglutinin - in
28	37	88.1	347	2 S52195	hemagglutinin - in
29	37	88.1	347	2 S52197	hemagglutinin - in

30	37	88.1	347	2 S52176	hemagglutinin - in
31	37	88.1	362	2 S38637	hemagglutinin - in
32	37	88.1	550	1 HMIV15	hemagglutinin prec
33	37	88.1	550	1 HMIV33	hemagglutinin prec
34	37	88.1	550	1 HMIV77	hemagglutinin prec
35	37	88.1	550	1 HMIV86	hemagglutinin prec
36	37	88.1	550	1 HMIV89	hemagglutinin prec
37	37	88.1	550	1 HMIVS2	hemagglutinin prec
38	37	88.1	550	1 HMIV21	hemagglutinin prec
39	37	88.1	550	1 HMIV80	hemagglutinin prec
40	37	88.1	550	1 HMIV98	hemagglutinin prec
41	37	88.1	550	1 HMIVS3	hemagglutinin prec
42	37	88.1	550	2 JQ1154	hemagglutinin prec
43	37	88.1	550	2 JQ1153	hemagglutinin prec
44	37	88.1	550	2 JQ1155	hemagglutinin prec
45	37	88.1	550	2 JQ1156	hemagglutinin prec

ALIGNMENTS

RESULT 1

S04605
Glycinin G3 - soybean
C;Species: Glycine max (soybean)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04605
R;Cho, T.J.; Nielsen, N.C.
Nucleic Acids Res. 17, 4388, 1989
A;Title: The glycinin Gy(3) gene from soybean.
A;Reference number: S04605; MUID:89296500; PMID:2740231
A;Accession: S04605
A;Molecule type: DNA
A;Residues: 1-481 <CHO>
A;Cross-references: UNIPROT:P11828; EMBL:X15123; NID:G18638; PIDN:CAA33217.1; PID:G1863
A;Experimental source: variety Dare
C;Genetics:
A;Gene: Gy3
A;Introns: 96/1; 177/3; 352/3
C;Superfamily: glycinin

Query Match 100.0%; Score 42; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
Db 57 PNNKPFQ 63

RESULT 2

S11003
Glycinin G3 precursor - soybean
C;Species: Glycine max (soybean)
C;Date: 21-Nov-1993 #sequence_revision 19-Jan-1996 #text_change 03-May-1996
C;Accession: S11003
R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallan, B.J.; Fischer, R.L.;
Plant Cell 1, 313-328, 1989
A;Title: Characterization of the glycinin gene family in soybean.
A;Reference number: S10851; MUID:92393391; PMID:2485233
A;Accession: S11003
A;Molecule type: DNA
A;Residues: 1-484 <NIE>
A;Experimental source: variety Dare
C;Genetics:
A;Gene: Gy3
C;Superfamily: glycinin
C;Keywords: storage protein
P;1-19/Domain: signal sequence #status predicted <SIG>
F;20-484/Product: glycinin G3 #status predicted <MAT>

Query Match 100.0%; Score 42; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.3;

RESULT 5

FW5YG2
glycinin chain AlaBx precursor - soybean
N;Alternate names: 11S globulin; glycinin AlaB1b
C;Species: Glycine max (soybean)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23497; MUID:86041867; PMID:2997720
R;Negoro, T.; Momma, T.; Fukazawa, C.
Nucleic Acids Res. 13, 6719-6731, 1985
A;Title: A cDNA clone encoding a glycinin A-1a subunit precursor of soybean.
A;Reference number: A23497; MUID:86041867; PMID:2997720
A;Accession: A23497
A;Molecule type: mRNA
A;Residues: 1-495 <NEG>
A;Cross-references: UNIPROT:P04776; GB:X02985; NID:G18614; PIDN:CAA26723.1; PID:G18615
A;Experimental source: cv. Bonminori
A;Note: the authors translated the codon AAC for residue 449 as Lys
A;Note: because of current nomenclature ambiguities, the authors choose to designate the
R;Kitamura, Y.; Arahira, M.; Itoh, Y.; Fukazawa, C.
Nucleic Acids Res. 18, 4245, 1990
A;Title: The complete nucleotide sequence of soybean glycinin A2B1a gene spanning to and
A;Reference number: S10502; MUID:90332420; PMID:2377465
A;Accession: S10502
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 481-495 <KIT>
A;Cross-references: EMBL:X53404; NID:G18522; PIDN:CAA37479.1; PID:G18523
C;Comment: The source of this protein was cotyledon tissue taken 38 days after flowering
C;Comment: By homology with the A2B1a component, residues 307-310, and 491-495 are removed
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-306/Product: glycinin chain Ala #status predicted <GLA>
F;311-490/Product: glycinin chain Bx #status predicted <GLB>
F;107-317/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PNNKPFQ 7
Db 57 PNNKPFQ 63

RESULT 6

glycinin G1 precursor - soybean
N;Alternate names: glycinin AlaBx
N;Contains: glycinin chain Ala, glycinin chain Bx
C;Species: Glycine max (soybean)
C;Date: 21-Nov-1993 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: S10851; S04603; JS0015
R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallan, B.J.; Fischer, R.L.; Plant Cell 1, 313-328, 1989
A;Title: Characterization of the glycinin gene family in soybean.
A;Reference number: S10851; MUID:92393391; PMID:2485233
A;Accession: S10851
A;Molecule type: DNA
A;Residues: 1-495 <NIE>
A;Cross-references: UNIPROT:P04776
A;Experimental source: variety Dare
R;Simb, T.L.; Goldberg, R.B.
Nucleic Acids Res. 17, 4386, 1989
A;Title: The glycinin Gy(1) gene from soybean.
A;Reference number: S04603; MUID:89296498; PMID:2740229
A;Accession: S04603
A;Molecule type: DNA
A;Residues: 1-495 <SIM>
A;Cross-references: EMBL:X15121; NID:G18634; PIDN:CAA33215.1; PID:G18635
A;Experimental source: variety Dare
R;Utsumi, S.; Kohno, M.; Mori, T.; Kito, M.

J. Agric. Food Chem. 35, 210-214, 1987
A;Title: An alternate cDNA encoding glycinin Ala Bx subunit.
A;Reference number: JS0015
A;Accession: JS0015
A;Molecule type: mRNA
A;Residues: 1-495 <UTS>
A;Experimental source: var. Shiotsurunoko
C;Genetics:
A;Gene: Gyl
A;Introns: 96/1; 180/3; 366/3
C;Superfamily: glycinin
C;Keywords: storage protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-495/Product: glycinin G1 #status predicted <MAT1>
F;311-495/Product: glycinin Ala chain #status predicted <MAT2>
F;311-495/Product: glycinin Bx chain #status predicted <MAT3>

Query Match 100.0%; Score 42; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PNNKPFQ 7
Db 57 PNNKPFQ 63

RESULT 7

HM1VE1
hemagglutinin precursor - influenza A virus (strain A/equine/Uruguay/1/63 [H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: Influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: A34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: A34064
A;Molecule type: Genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24718; GB:J04336; NID:G324024; PIDN:AAA43114.1; PID:G324025
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 100.0%; Score 42; DB 1; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PNNKPFQ 7
Db 304 PNNKPFQ 310

RESULT 8

JQ2375
hemagglutinin - influenza A virus (strain SN1389 and IN0190)
C;Species: Influenza A virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JQ2375; JQ2376
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A;Reference number: JQ2369; MUID:94065682; PMID:8245870
A;Accession: JQ2375

A:Molecule type: mRNA
A:Residues: 1-330 <ROC>
A:Cross-references: UNIPROT:Q7LZX9; GB:L20119
A:Experimental source: subtype H3N2
C:Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 330;
Best Local Similarity 85.7%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
||:||||
Db 290 PNDKPFQ 296

RESULT 9

hemagglutinin - influenza A virus (strain SN1289)
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JQ2374
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2369; MUID:94065682; PMID:8245870

A:Accession: JQ2374

A:Molecule type: mRNA

A:Residues: 1-330 <ROC>

A:Cross-references: UNIPROT:Q7LZY0; GB:L20115

A:Experimental source: subtype H3N2

C:Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 330;
Best Local Similarity 85.7%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
||:||||
Db 290 PNDKPFQ 296

RESULT 10

hemagglutinin - influenza A virus (strain HI0191)
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JQ2378
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2369; MUID:94065682; PMID:8245870

A:Accession: JQ2378

A:Molecule type: mRNA

A:Residues: 1-331 <ROC>

A:Cross-references: UNIPROT:Q7LZX7; GB:L20102

A:Experimental source: subtype H3N2

C:Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 331;
Best Local Similarity 85.7%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
||:||||
Db 291 PNDKPFQ 297

RESULT 11

hemagglutinin - influenza A virus (strain SD0191)
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JQ2377

R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2369; MUID:94065682; PMID:8245870

A:Accession: JQ2377

A:Molecule type: mRNA

A:Residues: 1-331 <ROC>

A:Cross-references: UNIPROT:Q7LZX8; GB:L20105

A:Experimental source: subtype H3N2

C:Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 331;
Best Local Similarity 85.7%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
||:||||
Db 291 PNDKPFQ 297

RESULT 12

hemagglutinin - influenza A virus (isolate A/England/68/94) (fragment)
C:Species: influenza A virus
A:Variety: isolate A/England/68/94
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: S52186
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula

A:Reference number: S52173

A:Accession: S52186

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: UNIPROT:Q82785; EMBL:Z46404; NID:G609045; PIDN:CAA86539.1; PID:G6090

A:Experimental source: isolate A/England/68/94

C:Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
||:||||
Db 289 PNDKPFQ 295

RESULT 13

hemagglutinin - influenza A virus (isolate A/England/1/93) (fragment)
C:Species: influenza A virus
A:Variety: isolate A/England/1/93
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: S52175
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula

A:Reference number: S52173

A:Accession: S52175

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: UNIPROT:Q82775; EMBL:Z46393; NID:G609024; PIDN:CAA86528.1; PID:G9405

A:Experimental source: isolate A/England/1/93

C:Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
||:||||
Db 289 PNDKPFQ 295

```
RESULT 14
S52187
hemagglutinin - influenza A virus (isolate A/England/7/94) (fragment)
C;Species: influenza A virus
A;Variety: isolate A/England/7/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S52187
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circulating
A;Reference number: S52173
A;Accession: S52187
A;Molecule type: mRNA
A;Residues: 1-347 <ELL>
A;Cross-references: UNIPROT:Q82786; EMBL:Z46405; NID:9609047; PIDN:CAA86540.1; PID:9609047
A;Experimental source: isolate A/England/7/94
C;Superfamily: influenza virus hemagglutinin

Query Match      88.1%; Score 37; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
Db 289 PNDKPFQ 295

RESULT 15
S52183
hemagglutinin - influenza A virus (isolate A/England/347/93) (fragment)
C;Species: influenza A virus
A;Variety: isolate A/England/347/93
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S52183
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circulating
A;Reference number: S52173
A;Accession: S52183
A;Molecule type: mRNA
A;Residues: 1-347 <ELL>
A;Cross-references: UNIPROT:Q82782; EMBL:Z46401; NID:9609039; PIDN:CAA86536.1; PID:9609039
A;Experimental source: isolate A/England/347/93
C;Superfamily: influenza virus hemagglutinin

Query Match      88.1%; Score 37; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
Db 289 PNDKPFQ 295

Search completed: November 6, 2004, 19:54:12
Job time : 18.0625 secs
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